

duplex.

28. (new) The method of claim 27, wherein said plurality includes duplexes of at least 10 distinct nucleic acid sequences.

29. (new) The method of claim 28, wherein said plurality includes at least 100 duplexes of distinct nucleic acid sequence.

30. (new) The method of claim 29, wherein said plurality includes at least 10,000 duplexes of distinct nucleic acid sequence.

31. (new) The method of claim 29, wherein said plurality includes at least 100,000 duplexes of distinct nucleic acid sequence.

32. (new) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a prokaryote.

33. (new) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a virus.

34. (new) The method of claim 27, wherein said plurality includes nucleic acid sequences derived from a eukaryote.

35. (new) The method of claim 34, wherein said eukaryote is a mammal.

36. (new) The method of claim 35, wherein said mammal is a human.

37. (new) The method of claim 36, wherein said plurality includes nucleic acid sequences derived from the coding region of a human gene.

38. (new) The method of claim 37, wherein said human gene is selected from the group consisting of: hemoglobin, dystrophin, BRCA1, BRCA2, CFTR, factor VIII, factor IX, oncogenes, tumor suppressors, and genes on human chromosome 21.

39. (new) The method of claim 27, wherein said mismatch in said duplex is a single nucleotide polymorphism.
40. (new) The method of claim 27, wherein said marker is inactivated by said *in vivo* mismatch corepair.
41. (new) The method of claim 27, wherein said marker is a recombinase.
42. (new) The method of claim 41, wherein said recombinase is Cre recombinase.
43. (new) The method of claim 27, wherein said bacterial cell characteristic is selected from the group consisting of: cell color, luminescence, antibiotic sensitivity, and antibiotic resistance.
44. (new) The method of claim 41, wherein mismatch corepair of said recombinase alters said bacterial cell's antibiotic resistance or sensitivity.
45. (new) The method of claim 27, further comprising the antecedent step of forming said plurality of DNA duplexes by annealing first nucleic acid strands, said first strands including at least one nucleic acid sequence, to second nucleic acid strands, said second strands including a plurality of distinct nucleic acid sequences.
46. (new) The method of claim 45, wherein said plurality of second nucleic acid strands are derived from a common source.
47. (new) The method of claim 46, wherein said common source is genomic DNA from a single individual.
48. (new) The method of claim 46, wherein said common source is cDNA from a single individual.
49. (new) The method of claim 45, wherein said plurality of second nucleic acid strands are derived from a pooled source.
50. (new) The method of claim 49, wherein said source is pooled from family members.